

SEQUENCE LISTING

<110> Genox Research, Inc.

National Center for Child Health and Development

<120> Methods for examination for allergic diseases, and
drugs for treating allergic diseases

<130> G1-A0211-US

<140>

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<150> JP 2002-193841

<151> 2002-07-02

<160> 14

<170> PatentIn Ver. 2.0

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<211> 2464

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (111).. (1904)

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Met Asp Leu Ala Ser Pro Glu Ala Ala Pro Ala Ala Pro Thr Ala Leu	
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Phe Leu Tyr Gln Leu Pro Gly Thr Val Gln Pro Cys Ser Ser Ala Ser	
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Ser Ser Ala Ser Ser Thr Ser Ser Ser Ser Ala Thr Ser Pro Ala Ser	
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Pro Leu Ser Gly Pro Val Asp Glu Ala Leu Ser Ser Ser Gly Ser Asp	
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Tyr Tyr Gly Ser Pro Cys Ser Ala Pro Ser Pro Ser Thr Pro Ser Phe	
135 140 145	

cag ccg ccc cag ctc tct ccc tgg gat ggc tcc ttc ggc cac ttc tcg 596
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 Lys Ala Ser Gly Pro Pro Gln Pro Pro Ala Phe Phe Ser Phe Ser Pro
 180 185 190

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 Ala Pro Gly Pro Ser Glu Gly Arg Cys Ala Val Cys Gly Asp Asn Ala
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 Ser Cys Gln His Tyr Gly Val Arg Thr Cys Glu Gly Cys Lys Gly Phe
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Arg Phe Gln Lys Cys Leu Ala Val Gly Met Val Lys Glu Val Val Arg	
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Thr Asp Ser Leu Lys Gly Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys	
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Gln Pro Pro Asp Ala Ser Pro Ala Asn Leu Leu Thr Ser Leu Val Leu	
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Ala His Leu Asp Ser Gly Pro Ser Thr Ala Lys Leu Asp Tyr Ser Lys	
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Phe Gln Glu Leu Val Leu Pro His Phe Gly Lys Glu Asp Ala Gly Asp	
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Val Gln Gln Phe Tyr Asp Leu Leu Ser Gly Ser Leu Glu Val Ile Arg	
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Lys Trp Ala Glu Lys Ile Pro Gly Phe Ala Glu Leu Ser Pro Ala Asp	
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 Thr Leu Pro Phe
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<212> PRT

<213> Homo sapiens

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 35 40 45

Ala Leu Pro Ser Phe Ser Thr Phe Met Asp Gly Tyr Thr Gly Glu Phe
 50 55 60

Asp Thr Phe Leu Tyr Gln Leu Pro Gly Thr Val Gln Pro Cys Ser Ser
 65 70 75 80

Ala Ser Ser Ser Ala Ser Ser Thr Ser Ser Ser Ser Ala Thr Ser Pro
 85 90 95

Ala Ser Ala Ser Phe Lys Phe Glu Asp Phe Gln Val Tyr Gly Cys Tyr
 100 105 110

Pro Gly Pro Leu Ser Gly Pro Val Asp Glu Ala Leu Ser Ser Ser Gly
 115 120 125

Ser Asp Tyr Tyr Gly Ser Pro Cys Ser Ala Pro Ser Pro Ser Thr Pro
 130 135 140

Ser Phe Gln Pro Pro Gln Leu Ser Pro Trp Asp Gly Ser Phe Gly His
 145 150 155 160

Phe Ser Pro Ser Gln Thr Tyr Glu Gly Leu Arg Ala Trp Thr Glu Gln
 165 170 175

Leu Pro Lys Ala Ser Gly Pro Pro Gln Pro Pro Ala Phe Phe Ser Phe
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Ser Pro Pro Thr Gly Pro Ser Pro Ser Leu Ala Gln Ser Pro Leu Lys
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Leu Phe Pro Ser Gln Ala Thr His Gln Leu Gly Glu Gly Glu Ser Tyr
 210 215 220

Ser Met Pro Thr Ala Phe Pro Gly Leu Ala Pro Thr Ser Pro His Leu
 225 230 235 240

Glu Gly Ser Gly Ile Leu Asp Thr Pro Val Thr Ser Thr Lys Ala Arg
 245 250 255

Ser Gly Ala Pro Gly Pro Ser Glu Gly Arg Cys Ala Val Cys Gly Asp
 260 265 270

Asn Ala Ser Cys Gln His Tyr Gly Val Arg Thr Cys Glu Gly Cys Lys
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Gly Phe Phe Lys Arg Thr Val Gln Lys Asn Ala Lys Tyr Ile Cys Leu
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Ala Asn Lys Asp Cys Pro Val Asp Lys Arg Arg Arg Asn Arg Cys Gln
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Phe Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Val Lys Glu Val
 325 330 335

Val Arg Thr Asp Ser Leu Lys Gly Arg Arg Gly Arg Leu Pro Ser Lys
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Pro Lys Gln Pro Pro Asp Ala Ser Pro Ala Asn Leu Leu Thr Ser Leu
 355 360 365

Val Leu Ala His Leu Asp Ser Gly Pro Ser Thr Ala Lys Leu Asp Tyr
 370 375 380

Ser Lys Phe Gln Glu Leu Val Leu Pro His Phe Gly Lys Glu Asp Ala
 385 390 395 400

Gly Asp Val Gln Gln Phe Tyr Asp Leu Leu Ser Gly Ser Leu Glu Val
 405 410 415

Ile Arg Lys Trp Ala Glu Lys Ile Pro Gly Phe Ala Glu Leu Ser Pro
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Ala Asp Gln Asp Leu Leu Leu Glu Ser Ala Phe Leu Glu Leu Phe Ile
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Leu Arg Leu Ala Tyr Arg Ser Lys Pro Gly Glu Gly Lys Leu Ile Phe
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Cys Ser Gly Leu Val Leu His Arg Leu Gln Cys Ala Arg Gly Phe Gly
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Asp Trp Ile Asp Ser Ile Leu Ala Phe Ser Arg Ser Leu His Ser Leu
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Thr Asp Arg His Gly Leu Gln Glu Pro Arg Arg Val Glu Glu Leu Gln
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Asn Arg Ile Ala Ser Cys Leu Lys Glu His Val Ala Ala Val Ala Gly
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Glu Leu Arg Thr Leu Cys Thr Gln Gly Leu Gln Arg Ile Phe Tyr Leu
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Met Asp Thr Leu Pro Phe
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gcccgggctc ccagagggaa ctgcacttcg gcagagttga atgaatgaag agagacgcgg 180

agaactccta aggaggagat tggacaggct ggactcccca ttgcttttct aaaaatcttg 240

gaaactttgt ctttcattga attacgacac tgtccacett taatttcctc gaaaacgcct 300

gtaactcggc tgaagcc atg cct tgt gtt cag gcg cag tat ggg tcc tcg 350

Met Pro Cys Val Gln Ala Gln Tyr Gly Ser Ser

1

5

10

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Pro Gln Gly Ala Ser Pro Ala Ser Gln Ser Tyr Ser Tyr His Ser Ser

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Phe Ser Thr Phe Met Asp Asn Tyr Ser Thr Gly Tyr Asp Val Lys Pro	
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cct tgc ttg tac caa atg ccc ctg tcc gga cag cag tcc tcc att aag	590
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gta gaa gac att cag atg cac aac tac cag caa cac agc cac ctg ccc	638
Val Glu Asp Ile Gln Met His Asn Tyr Gln Gln His Ser His Leu Pro	
95 100 105	
ccc cag tct gag gag atg atg ccg cac tcc ggg tcg gtt tac tac aag	686
Pro Gln Ser Glu Glu Met Met Pro His Ser Gly Ser Val Tyr Tyr Lys	
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Pro Ser Ser Pro Pro Thr Pro Thr Thr Pro Gly Phe Gln Val Gln His	
125 130 135	
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Ser Pro Met Trp Asp Asp Pro Gly Ser Leu His Asn Phe His Gln Asn	
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Tyr Val Ala Thr Thr His Met Ile Glu Gln Arg Lys Thr Pro Val Ser	
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Arg Leu Ser Leu Phe Ser Phe Lys Gln Ser Pro Pro Gly Thr Pro Val	
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Ser Ser Cys Gln Met Arg Phe Asp Gly Pro Leu His Val Pro Met Asn	
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Pro Glu Pro Ala Gly Ser His His Val Val Asp Gly Gln Thr Phe Ala	
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Gln Ile Gly His Ala Ser Gln Leu Leu Asp Thr Gln Val Pro Ser Pro	
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Lys Gly Phe Phe Lys Arg Thr Val Gln Lys Asn Ala Lys Tyr Val Cys	
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Leu Ala Asn Lys Asn Cys Pro Val Asp Lys Arg Arg Arg Asn Arg Cys	
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Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Val Lys Glu	
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Leu Ile Ser Ala Leu Val Arg Ala His Val Asp Ser Asn Pro Ala Met	
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Thr Ser Leu Asp Tyr Ser Arg Phe Gln Ala Asn Pro Asp Tyr Gln Met	
380 385 390 395	
agt gga gat gac acc cag cat atc cag caa ttc tat gat ctc ctg act	1550
Ser Gly Asp Asp Thr Gln His Ile Gln Gln Phe Tyr Asp Leu Leu Thr	
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Gly Ser Met Glu Ile Ile Arg Gly Trp Ala Glu Lys Ile Pro Gly Phe	
415 420 425	
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Ala Asp Leu Pro Lys Ala Asp Gln Asp Leu Leu Phe Glu Ser Ala Phe	
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aac ttg cag aat atg aac atc gac att tct gcc ttc tcc tgc att gct 1838
 Asn Leu Gln Asn Met Asn Ile Asp Ile Ser Ala Phe Ser Cys Ile Ala
 495 500 505

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cgc att ttc tac ctg aaa ttg gaa gac ttg gtg cca ccg cca gca ata 2078
 Arg Ile Phe Tyr Leu Lys Leu Glu Asp Leu Val Pro Pro Pro Ala Ile
 575 580 585

att gac aaa ctt ttc ctg gac act tta cct ttc taagacctcc tcccaagcac 2131
 Ile Asp Lys Leu Phe Leu Asp Thr Leu Pro Phe
 590 595

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<211> 598

<212> PRT

<213> Homo sapiens

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Thr Glu Ile Thr Ala Thr Thr Ser Leu Pro Ser Phe Ser Thr Phe Met
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Asp Asn Tyr Ser Thr Gly Tyr Asp Val Lys Pro Pro Cys Leu Tyr Gln
65 70 75 80

Met Pro Leu Ser Gly Gln Gln Ser Ser Ile Lys Val Glu Asp Ile Gln
85 90 95

Met His Asn Tyr Gln Gln His Ser His Leu Pro Pro Gln Ser Glu Glu
100 105 110

Met Met Pro His Ser Gly Ser Val Tyr Tyr Lys Pro Ser Ser Pro Pro
115 120 125

Thr Pro Thr Thr Pro Gly Phe Gln Val Gln His Ser Pro Met Trp Asp

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His Met Ile Glu Gln Arg Lys Thr Pro Val Ser Arg Leu Ser Leu Phe		
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Ser Phe Lys Gln Ser Pro Pro Gly Thr Pro Val Ser Ser Cys Gln Met		
	180	185 190
Arg Phe Asp Gly Pro Leu His Val Pro Met Asn Pro Glu Pro Ala Gly		
	195	200 205
Ser His His Val Val Asp Gly Gln Thr Phe Ala Val Pro Asn Pro Ile		
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Arg Lys Pro Ala Ser Met Gly Phe Pro Gly Leu Gln Ile Gly His Ala		
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Ser Gln Leu Leu Asp Thr Gln Val Pro Ser Pro Pro Ser Arg Gly Ser		
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Pro Ser Asn Glu Gly Leu Cys Ala Val Cys Gly Asp Asn Ala Ala Cys		
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Gln His Tyr Gly Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys		
	275	280 285
Arg Thr Val Gln Lys Asn Ala Lys Tyr Val Cys Leu Ala Asn Lys Asn		
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Cys Pro Val Asp Lys Arg Arg Arg Asn Arg Cys Gln Tyr Cys Arg Phe		
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Gln Lys Cys Leu Ala Val Gly Met Val Lys Glu Val Val Arg Thr Asp		

325	330	335
Ser Leu Lys Gly Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro		
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Gln Glu Pro Ser Pro Pro Ser Pro Pro Val Ser Leu Ile Ser Ala Leu		
355	360	365
Val Arg Ala His Val Asp Ser Asn Pro Ala Met Thr Ser Leu Asp Tyr		
370	375	380
Ser Arg Phe Gln Ala Asn Pro Asp Tyr Gln Met Ser Gly Asp Asp Thr		
385	390	395
Gln His Ile Gln Gln Phe Tyr Asp Leu Leu Thr Gly Ser Met Glu Ile		
405	410	415
Ile Arg Gly Trp Ala Glu Lys Ile Pro Gly Phe Ala Asp Leu Pro Lys		
420	425	430
Ala Asp Gln Asp Leu Leu Phe Glu Ser Ala Phe Leu Glu Leu Phe Val		
435	440	445
Leu Arg Leu Ala Tyr Arg Ser Asn Pro Val Glu Gly Lys Leu Ile Phe		
450	455	460
Cys Asn Gly Val Val Leu His Arg Leu Gln Cys Val Arg Gly Phe Gly		
465	470	475
Glu Trp Ile Asp Ser Ile Val Glu Phe Ser Ser Asn Leu Gln Asn Met		
485	490	495
Asn Ile Asp Ile Ser Ala Phe Ser Cys Ile Ala Ala Leu Ala Met Val		
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Gly Leu Asn Arg Pro Asn Tyr Leu Ser Lys Leu Leu Gly Lys Leu Pro		
545	550	555 560
Glu Leu Arg Thr Leu Cys Thr Gln Gly Leu Gln Arg Ile Phe Tyr Leu		
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<210> 6

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Synthesized Primer Sequence

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Synthesized Probe Sequence

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<221> misc_binding

<222> (30)

<223> Label TAMRA

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30

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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20

<210> 9

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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24

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Probe Sequence

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24

<210> 11

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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ttt

63

<210> 12

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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25

<210> 13

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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25

<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence

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<222> (1)

<223> Label FAM

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26